

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2007; month=12; day=18; hr=19; min=6; sec=13; ms=388;]

=====

Application No: 10695577 Version No: 2.0

Input Set:

Output Set:

Started: 2007-12-03 12:22:33.045
Finished: 2007-12-03 12:22:33.758
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 713 ms
Total Warnings: 0
Total Errors: 0
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

SEQUENCE LISTING

<110> Chapman, Edwin R.
Dong, Min

<120> BOTULINUM NEUROTOXIN B RECEPTORS AND USE THEREOF

<130> 960296.99004

<140> 10695577

<141> 2003-10-28

<150> 60/422,951

<151> 2002-10-31

<150> 60/498,128

<151> 2003-08-27

<160> 10

<170> PatentIn version 3.3

<210> 1

<211> 2381

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (525)..(1790)

<220>

<221> misc_feature

<222> (618)..(680)

<223> BoNT/B binding domain

<220>

<221> misc_feature

<222> (681)..(761)

<223> Gangliosides binding domain or transmembrane domain

<400> 1

accggggcaa gcccccaggg tctgtctcac ccaacagggg gtcagggtcc ccgaagtgtg 60

tgcagggcg ggccggccag ctgggaccag ctggtgcccc tagaaaacct cacccacacc 120

cacacccaca cacccctttt gtgttgagg ctgcccctct gagagcggag gcagcgagag 180

agtactcggt tgccctcgac cggccgcgg tgagagcagc ggggaccaag actcgaccca 240

tctcccggtc ggtccctcgct ccagttccc tctgaatcct acacttcata tgttagacacc 300

ttactcaact ggcatttgtt agtcaagtct cctctgcattc caaggaaaag aagactttgg 360

cgcgctcgaa caaccaacat aagcagtctg atcagaagac attcaaattg ccgtcccgag 420

agctccagca gaacatctcg ttaagattga agaaaggaga ttccaaaagg acaaaaaacc		480	
caaatactcc agactacccc cagcagacat ccgctgaacc aaaa atg gtg agt gcc	Met Val Ser Ala	536	
	1		
agt cgt cct gag gcc ctg gct gcc cct gtc acc act gtt gcg acc ctt		584	
Ser Arg Pro Glu Ala Leu Ala Ala Pro Val Thr Thr Val Ala Thr Leu			
5	10	15	20
gtc cca cac aac gcc act gag cca gcc agt cct ggg gaa ggg aag gaa		632	
Val Pro His Asn Ala Thr Glu Pro Ala Ser Pro Gly Glu Gly Lys Glu			
25	30	35	
gat gcc ttt tcc aag ctg aag cag aag ttt atg aat gaa ctg cat aaa		680	
Asp Ala Phe Ser Lys Leu Lys Gln Lys Phe Met Asn Glu Leu His Lys			
40	45	50	
atc cca ttg cca ccg tgg gcc tta att gcc ata gcc ata gtt gcg gtc		728	
Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile Ala Ile Val Ala Val			
55	60	65	
ctt cta gtc gtg acc tgc tgc ttc tgt gtc tgt aag aaa tgt ttg ttc		776	
Leu Leu Val Val Thr Cys Cys Phe Cys Val Cys Lys Cys Leu Phe			
70	75	80	
aaa aag aaa aac aag aag gga aag gaa aag gga ggg aag aac gcc		824	
Lys Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys Gly Gly Lys Asn Ala			
85	90	95	100
att aac atg aaa gac gtg aaa gac tta ggg aag acc atg aag gat cag		872	
Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys Thr Met Lys Asp Gln			
105	110	115	
gcc ctt aag gat gac gat gct gaa act gga ctg act gat gga gaa gaa		920	
Ala Leu Lys Asp Asp Asp Ala Glu Thr Gly Leu Thr Asp Gly Glu Glu			
120	125	130	
aag gag gag ccc aag gaa gag gag aaa ctg gga aag ctt caa tat tca		968	
Lys Glu Glu Pro Lys Glu Glu Lys Leu Gly Lys Leu Gln Tyr Ser			
135	140	145	
ctg gac tat gac ttc cag aat aac cag ctg ctg gtg gga atc atc cag		1016	
Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu Val Gly Ile Ile Gln			
150	155	160	
gct gct gaa ctg ccc gcc ctg gac atg gga ggc aca tct gat cca tac		1064	
Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr			
165	170	175	180
gtc aaa gtc ttc ctg ctg ccc gac aaa aag aag aag ttt gag aca aaa		1112	
Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Phe Glu Thr Lys			
185	190	195	
gtc cac cgg aaa acc ctc aat cca gtc ttc aat gaa cag ttt act ttc		1160	
Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu Gln Phe Thr Phe			

200	205	210	
aag gtg cca tac tcg gaa tta ggt ggc aag aca ctg gtg atg gct gtg Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu Val Met Ala Val			1208
215	220	225	
tat gat ttt gac cgc ttc tcc aag cac gac atc att gga gag ttc aaa Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Phe Lys			1256
230	235	240	
gtt cct atg aac acc gtg gat ttt ggc cac gtc acc gag gag tgg cgc Val Pro Met Asn Thr Val Asp Phe Gly His Val Thr Glu Glu Trp Arg			1304
245	250	255	260
gat ctc cag agt gct gag aaa gaa gag caa gag aaa ctg ggt gac atc Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu Lys Leu Gly Asp Ile			1352
265	270	275	
tgc ttc tcc ctc cgc tac gtc cct act gcc ggc aag ctg act gtt gtc Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys Leu Thr Val Val			1400
280	285	290	
att ctg gaa gcc aag aac ctg aag aag atg gat gtg ggt ggc tta tct Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val Gly Gly Leu Ser			1448
295	300	305	
gat ccc tat gta aag att cac ctg atg cag aac ggc aag aga ctg aag Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn Gly Lys Arg Leu Lys			1496
310	315	320	
aag aaa aag aca acg att aag aag aac aca ctt aac ccc tac tac aat Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn			1544
325	330	335	340
gag tcc ttc agc ttt gaa gtt ccg ttc gag caa atc cag aaa gtg caa Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln Ile Gln Lys Val Gln			1592
345	350	355	
gtg gtg gta act gtt ttg gac tat gac aag att ggc aag aac gac gcc Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile Gly Lys Asn Asp Ala			1640
360	365	370	
atc ggc aaa gtc ttt gtg ggc tac aac agc acc ggc gca gag ctg cga Ile Gly Lys Val Phe Val Gly Tyr Asn Ser Thr Gly Ala Glu Leu Arg			1688
375	380	385	
cac tgg tca gac atg ctg gcc aac ccc cgg cga ccc atc gcc cag tgg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro Ile Ala Gln Trp			1736
390	395	400	
cac act ctg cag gta gag gag gat gtc atg ctg gct gtc aag His Thr Leu Gln Val Glu Glu Val Asp Ala Met Leu Ala Val Lys			1784
405	410	415	420
aag taa agggaaaaag aaggctttct gcgtctgcc acgttagtgct cttagccag Lys			1840

tatctgtaaa tacctcagta atatgggtcc tttcagtttc cagccatgca ttccctgatac	1900
aatccagtgg tacttcagat cctgttttaa tttgcacaaa tttaagtgt aaaaaggcccct	1960
atgcccttca tcataccact gccctccaaa tctacttttc tttaagcaa tatgtatgtgt	2020
agatagagca tgactgaaat gtattgtatc acaccgttgt atataccagt atgctaaaga	2080
tttatttcta gtttgtgtat ttgtatgttg taagcgtttc ctaatctgtg tataatctaga	2140
tgttttaat aagatgttct attttaaact atgtaaattg actgagatat aggagaactg	2200
ataatataatt atatggtaaa tatagtatcg tctgcattcc agcaaaaata tcaatttgaa	2260
aggcactagt acagttAAC caacatctta aaggacaact taaacctgaa ctttctattg	2320
aatccttga gtaccaagat ttgctcacac gacatcttg atgggtgaac ccaattttgt	2380
a	2381

<210> 2
<211> 421
<212> PRT
<213> Mus musculus

<400> 2

Met Val Ser Ala Ser Arg Pro Glu Ala Leu Ala Ala Pro Val Thr Thr			
1	5	10	15

Val Ala Thr Leu Val Pro His Asn Ala Thr Glu Pro Ala Ser Pro Gly		
20	25	30

Glu Gly Lys Glu Asp Ala Phe Ser Lys Leu Lys Gln Lys Phe Met Asn		
35	40	45

Glu Leu His Lys Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile Ala		
50	55	60

Ile Val Ala Val Leu Leu Val Val Thr Cys Cys Phe Cys Val Cys Lys			
65	70	75	80

Lys Cys Leu Phe Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys Gly		
85	90	95

Gly Lys Asn Ala Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys Thr		
100	105	110

Met Lys Asp Gln Ala Leu Lys Asp Asp Asp Ala Glu Thr Gly Leu Thr
115 120 125

Asp Gly Glu Glu Lys Glu Glu Pro Lys Glu Glu Glu Lys Leu Gly Lys
130 135 140

Leu Gln Tyr Ser Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu Val
145 150 155 160

Gly Ile Ile Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr
165 170 175

Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys
180 185 190

Phe Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu
195 200 205

Gln Phe Thr Phe Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu
210 215 220

Val Met Ala Val Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile
225 230 235 240

Gly Glu Phe Lys Val Pro Met Asn Thr Val Asp Phe Gly His Val Thr
245 250 255

Glu Glu Trp Arg Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu Lys
260 265 270

Leu Gly Asp Ile Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys
275 280 285

Leu Thr Val Val Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val
290 295 300

Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn Gly
305 310 315 320

Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu Asn
325 330 335

Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln Ile

340

345

350

Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile Gly
355 360 365

Lys Asn Asp Ala Ile Gly Lys Val Phe Val Gly Tyr Asn Ser Thr Gly
370 375 380

Ala Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro
385 390 395 400

Ile Ala Gln Trp His Thr Leu Gln Val Glu Glu Glu Val Asp Ala Met
405 410 415

Leu Ala Val Lys Lys
420

<210> 3
<211> 4654
<212> DNA
<213> Rattus rattus

<220>
<221> CDS
<222> (526)..(1791)

<220>
<221> misc_feature
<222> (619)..(681)
<223> BoNT/B binding domain

<220>
<221> misc_feature
<222> (682)..(762)
<223> Gangliosides binding domain or transmembrane domain

<400> 3
ctctgaccga gttcagcccc cagtgtcttt cctccacactc ctctgcagc ggcagcatcg 60
gcagttggca gtgggcaact tgaggctgta accagggcaa gcccccaaggg tcctgctcac 120
ccgacagggg gtcagactcc ccaaagggggt gtgtgcaggg cgggggcggc cagctggac 180
cagctggtgg ccctagaaaa cctcacccac acccacacac cccttttgtt ttgcaggctg 240
cccctctgag agcggaggca gcgagagtac tcgcgtgcct cgacccggtc cgcggtgaga 300
gctgcggggga ccaagactcg caccacactcc cggtcctcgc tccaggaaaa gaagacttga 360
aagtgcgttga gcaaccaaca tccgcagtca gatcgaaaga ctctgccctg gccatcccc 420

200	205	210	
aag gta ccc tac tcg gaa tta ggt ggc aaa acc ctg gtg atg gct gtg Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu Val Met Ala Val			1209
215	220	225	
tat gac ttt gat cgc ttc tcc aag cac gac atc atc gga gag ttc aaa Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Phe Lys			1257
230	235	240	
gtt cct atg aac acc gtg gat ttt ggc cat gtg acc gag gag tgg cgc Val Pro Met Asn Thr Val Asp Phe Gly His Val Thr Glu Glu Trp Arg			1305
245	250	255	260
gat ctc cag agc gct gag aaa gaa gag caa gag aaa ctg ggt gac atc Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu Lys Leu Gly Asp Ile			1353
265	270	275	
tgc ttc tcc ctc cgc tac gtc cct act gcc ggc aaa ctg act gtt gtc Cys Phe Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys Leu Thr Val Val			1401
280	285	290	
att ctg gaa gcc aag aac ctg aag aag atg gat gtg ggt ggc tta tct Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val Gly Gly Leu Ser			1449
295	300	305	
gat ccc tac gtg aag att cac ctg atg cag aac ggt aag agg ctg aag Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn Gly Lys Arg Leu Lys			1497
310	315	320	
aag aaa aag acg acg att aag aag aac aca ctc aac ccc tac tac aac Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn			1545
325	330	33	